



NCBI

Nucleotide

Protein

Translations

Retrieve results for an RID

protein-protein **BLAST**

HTHQDFQPVHLVALNTPLS

[Search](#)

Set subsequence From: _____ To: _____

Choose database nrDo CD-Search ☒Now: **BLAST!** or **Reset query** **Reset all****Options** for advanced blasting

Limit by entrez query _____ or select from: (none)

Composition-based statistics ☒Choose filter ☐ Low complexity ☐ Mask for lookup table only ☐ Mask lower caseExpect 10Word Size 3Matrix BLOSUM62 Gap Costs Existence: 11 Extension: 1[PSSM](#)

Other advanced _____

PHI pattern _____

EXHIBIT

A-1

FormatShow ☒ Graphical Overview ☒ NCBI-gi Alignment ☐ in HTML ☐ formatNumber of: Descriptions 100 ☐ Alignments 50 ☐Alignment view Pairwise ☐Format for PSI-BLAST ☐ with inclusion threshold: 0.001 ☐Layout: Two Windows ☐ Formatting options on page with results: None ☐Autoformat Semi-auto ☐Send results by e-mail **BLAST!** or **Reset all**Get the URL with preset values ? **Get URL**



results of BLAST

BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 997977704-13946-4068

Query=

(20 letters)

Database: nr

736,524 sequences; 233,319,389 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 20 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:		Score (bits)	E Value
gi 7446031 pir A56101	collagen alpha 1(XVIII) chain precur...	48	2e-05
gi 2137133 pir S72490	alpha 1(XVIII) collagen - mouse (fra...	48	2e-05
gi 13937351 ref NP_034059.1	procollagen, type XVIII, alpha...	48	2e-05
gi 539809 pir PN0675	collagen alpha 1(XVIII) chain - mouse...	48	2e-05
gi 12644252 sp P39061 CA1H MOUSE	COLLAGEN ALPHA 1(XVIII) CH...	47	5e-05
gi 7739777 gb AAF69009.1	(AF257775) endostatin [Mus musculus]	46	7e-05
gi 13096461 cds 1DY1.A	Chain A, Murine Endostatin, Crystal ...	46	8e-05
gi 1083262 pir A54072	collagen alpha 1(XVIII) chain - mous...	46	9e-05
gi 1167906 gb AAC52903.1	(U03715) alpha-1(XVIII) collagen ...	46	1e-04
gi 7446033 pir B54101	collagen alpha 1(XVIII) chain precur...	46	1e-04
gi 2920537 gb AAC39659.1	(AF018082) type XVIII collagen [H...	43	6e-04
gi 6007583 gb AAF00975.1	AF189709 1 (AF189709) collagen XVI...	43	7e-04
gi 1082300 pir A53019	collagen alpha 1(XVIII) chain - huma...	43	8e-04

EXHIBIT

A-3

gi 13385620 ref NP_085059.1	collagen, type XVIII, alpha 1;...	42	0.001
gi 7717447 emb CAB90481.1	(AL163302) human type XVIII coll...	42	0.001
gi 6013265 gb AAAF01310.1	(AF184060) type XVIII collagen [H...	42	0.002
gi 3891932 pdb 1BNL:A	Chain A, Zinc Dependent Dimers Observ...	41	0.002
gi 14780774 ref XP_016106.2	collagen, type XVIII, alpha [H...	40	0.004
gi 3493143 gb AAC33294.1	(AF083440) collagen XVIII [Gallus...	40	0.005
gi 4558170 pdb 1KOE	Endostatin	33	0.80

Alignments

>gi|7446031|pir|A56101 collagen alpha 1(XVIII) chain precursor, short splice form - mouse
Length = 1315

Score = 48.1 bits (113), Expect = 2e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS
Sbjct: 1132 HTHQDFQPVHLHLVALNTPLS 1151

>gi|2137133|pir|S72450 alpha 1(XVIII) collagen - mouse (fragment)
gi|511298|gb|AAA19787.1 (L22545) alpha 1(XVIII) collagen [Mus musculus]
Length = 1288

Score = 48.1 bits (113), Expect = 2e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS
Sbjct: 1105 HTHQDFQPVHLHLVALNTPLS 1124

>gi|13937351|ref|NP_034059.1 procollagen, type XVIII, alpha 1 [Mus musculus]
gi|1167905|gb|AAC52901.1 (U03715) alpha-1(XVIII) collagen [Mus musculus]
Length = 1315

Score = 48.1 bits (113), Expect = 2e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS
Sbjct: 1132 HTHQDFQPVHLHLVALNTPLS 1151

>gi|539809|pir|PN0675 collagen alpha 1(XVIII) chain - mouse (fragment)
gi|467517|dbj|BAA04483.1 (D17546) Collagen [Mus musculus]
Length = 1140

Score = 48.1 bits (113), Expect = 2e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS
Sbjct: 957 HTHQDFQPVHLHLVALNTPLS 976

>gi|12644252|sp|P39061|CA1H MOUSE COLLAGEN ALPHA 1(XVIII) CHAIN PRECURSOR [CONTAINS: ENDOSTATIN]
gi|1167907|gb|AA252902.1 (U03715) alpha-1(XVIII) collagen [Mus musculus]
Length = 1527

Score = 46.6 bits (109), Expect = 5e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS
Sbjct: 1344 HTHQDFQPVHLHLVALNTPLS 1363

>gi|7739777|gb|AAF63009.1 (AF257775) endostatin [Mus musculus]
Length = 184

Score = 46.2 bits (108), Expect = 7e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20
HTHQDFQPVHLHLVALNTPLS



Sbjct: 1 HTHQDFQPVHLHLVALNTPLS 20

>gi|13096461|pdb|1DY1|A Chain A, Murine Endostatin, Crystal Form Iii
gi|7767124|pdb|1DY0|A Chain A, Murine Endostatin, Crystal Form Ii
Length = 188

Score = 45.8 bits (107), Expect = 8e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

HTHQDFQPVHLHLVALNTPLS

Sbjct: 5 HTHQDFQPVHLHLVALNTPLS 24

>gi|1083262|pir|A54072 collagen alpha 1(XVIII) chain - mouse (fragment)
gi|487734|gb|AAA20657.1| (U03714) alpha 1(XVIII) collagen [Mus musculus]
Length = 482

Score = 45.8 bits (107), Expect = 9e-05
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

HTHQDFQPVHLHLVALNTPLS

Sbjct: 299 HTHQDFQPVHLHLVALNTPLS 318

>gi|1167906|gb|AAC52903.1| (U03715) alpha-1(XVIII) collagen [Mus musculus]
Length = 1774

Score = 45.8 bits (107), Expect = 1e-04
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

HTHQDFQPVHLHLVALNTPLS

Sbjct: 1591 HTHQDFQPVHLHLVALNTPLS 1610

>gi|7446033|pir|B56101 collagen alpha 1(XVIII) chain precursor, long splice form - mouse
Length = 1774

Score = 45.8 bits (107), Expect = 1e-04
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

HTHQDFQPVHLHLVALNTPLS

Sbjct: 1591 HTHQDFQPVHLHLVALNTPLS 1610

>gi|2920537|gb|AAC39659.1| (AF018082) type XVIII collagen [Homo sapiens]
Length = 1336

Score = 43.1 bits (100), Expect = 6e-04
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

H+H+DFQPVHLHLVALN+PLS

Sbjct: 1154 HSHRDFQPVHLHLVALNSPLS 1173

>gi|6007583|gb|AAF00975.1|AF189709.1 (AF189709) collagen XVIII [Rattus norvegicus]
Length = 226

Score = 43.1 bits (100), Expect = 7e-04
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20

HTHQDF PVLHLVALNTPLS

Sbjct: 43 HTHQDFHPVHLHLVALNTPLS 62

>gi|1082300|pir|A53019 collagen alpha 1(XVIII) chain - human (fragment)
gi|562794|gb|AAA51864.1| (L22548) collagen type XVIII alpha 1 [Homo sapiens]
Length = 684

Score = 42.7 bits (99), Expect = 8e-04
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVHLHLVALNTPLS 20



H+H+DFQPVLHLVALN+PLS
Sbjct: 502 HSHRDFQPVLHLVALNSPLS 521

>gi|13385620|ref|NP_085059.1| collagen, type XVIII, alpha 1; endostatin [Homo sapiens]
gi|12644251|sp|P39060|CA1H HUMAN COLLAGEN ALPHA 1(XVIII) CHAIN PRECURSOR [CONTAINS: ENDOSTATIN]
gi|2920535|gb|AAC39658.1| (AF018081) type XVIII collagen [Homo sapiens]
Length = 1516

Score = 42.0 bits (97), Expect = 0.001
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 1334 HSHRDFQPVLHLVALNSPLS 1353

>gi|7717447|emb|CAB90482.1| (AL163302) human type XVIII collagen [Homo sapiens]
Length = 1519

Score = 42.0 bits (97), Expect = 0.001
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 1337 HSHRDFQPVLHLVALNSPLS 1356

>gi|6013265|gb|AAF01310.1| (AF184060) type XVIII collagen [Homo sapiens]
Length = 184

Score = 41.6 bits (96), Expect = 0.002
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 2 HSHRDFQPVLHLVALNSPLS 21

>gi|3891932|pdb|1BNL|A Chain A, Zinc Dependent Dimers Observed In Crystals Of Human
Endostatin
gi|3891933|pdb|1BNL|B Chain B, Zinc Dependent Dimers Observed In Crystals Of Human
Endostatin
gi|3891934|pdb|1BNL|C Chain C, Zinc Dependent Dimers Observed In Crystals Of Human
Endostatin
gi|3891935|pdb|1BNL|D Chain D, Zinc Dependent Dimers Observed In Crystals Of Human
Endostatin
Length = 178

Score = 41.2 bits (95), Expect = 0.002
Identities = 17/20 (85%), Positives = 19/20 (95%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 1 HSHRDFQPVLHLVALNAPLS 20

>gi|14780774|ref|XP_016106.2| collagen, type XVIII, alpha [Homo sapiens]
Length = 525

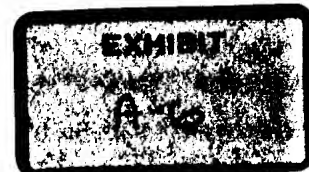
Score = 40.4 bits (93), Expect = 0.004
Identities = 17/20 (85%), Positives = 20/20 (100%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 343 HSHRDFQPVLHLVALNSPLS 362

>gi|3493143|gb|AAC33294.1| (AF082440) collagen XVIII [Gallus gallus]
Length = 386

Score = 40.0 bits (92), Expect = 0.005
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 HTHQDFQPVLHLVALNTPLS 20
H+H+DFQPVLHLVALN+PLS
Sbjct: 203 HSHRDFQPVLHLVALNSPLS 222



>gi_4558170|pdb_1KOE| Endostatin
Length = 172

Score = 32.7 bits (73), Expect = 0.80
Identities = 14/14 (100%), Positives = 14/14 (100%)

Query: 7 QPVLHLVALNTPLS 20
QPVLHLVALNTPLS
Sbjct: 1 QPVLHLVALNTPLS 14

Database: nr
Posted date: Aug 14, 2001 9:05 PM
Number of letters in database: 233,319,389
Number of sequences in database: 736,524

Lambda	K	H
0.323	0.135	0.423

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 9,201,175
Number of Sequences: 736524
Number of extensions: 89568
Number of successful extensions: 395136991356
Number of sequences better than 10.0: 268722324
Number of HSP's better than 10.0 without gapping: 20
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 104
Number of HSP's gapped (non-prelim): 20
length of query: 20
length of database: 233,319,389
effective HSP length: 0
effective length of query: 24
effective length of database: 233,319,389
effective search space: 5599665336
effective search space used: 5599665336
T: 11
A: 40
X1: 16 (7.5 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 64 (29.3 bits)

EXHIBIT